

FIG. 1

10026065 "120701

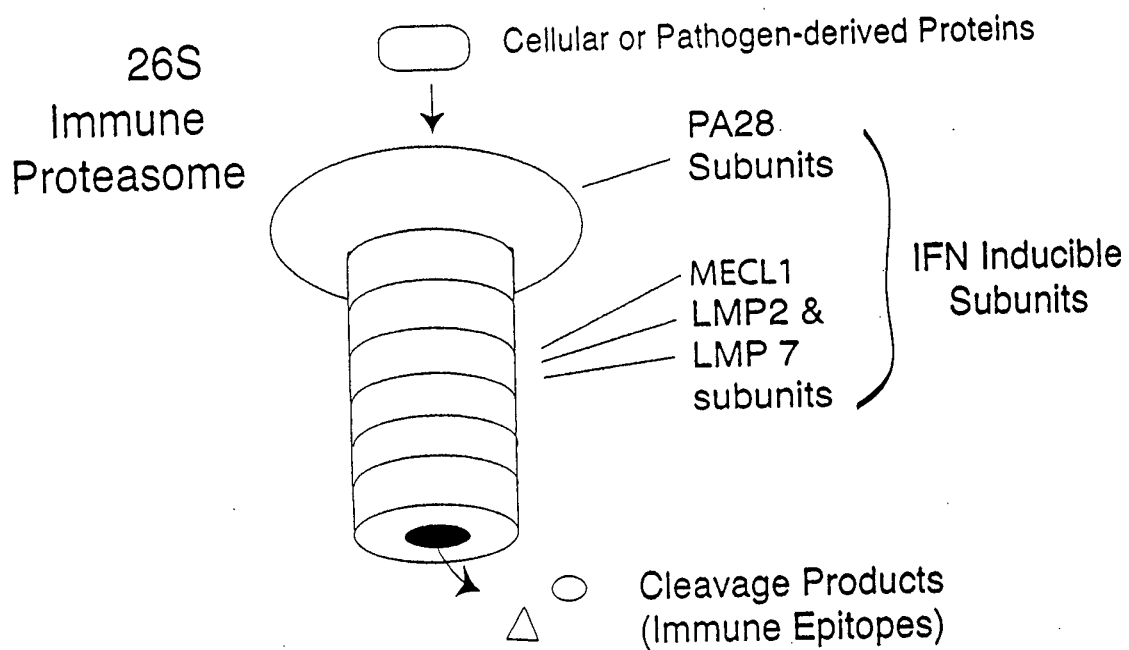
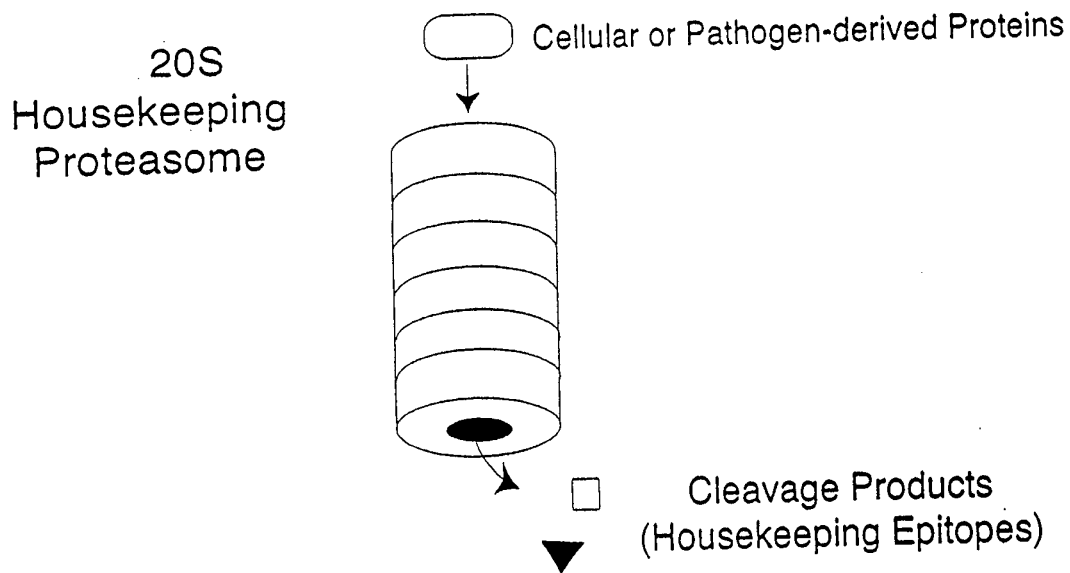


FIG. 2

"Antigen Synchronization" Between Infected Cell and APC Results in T cell Response That Recognizes Virus Epitope

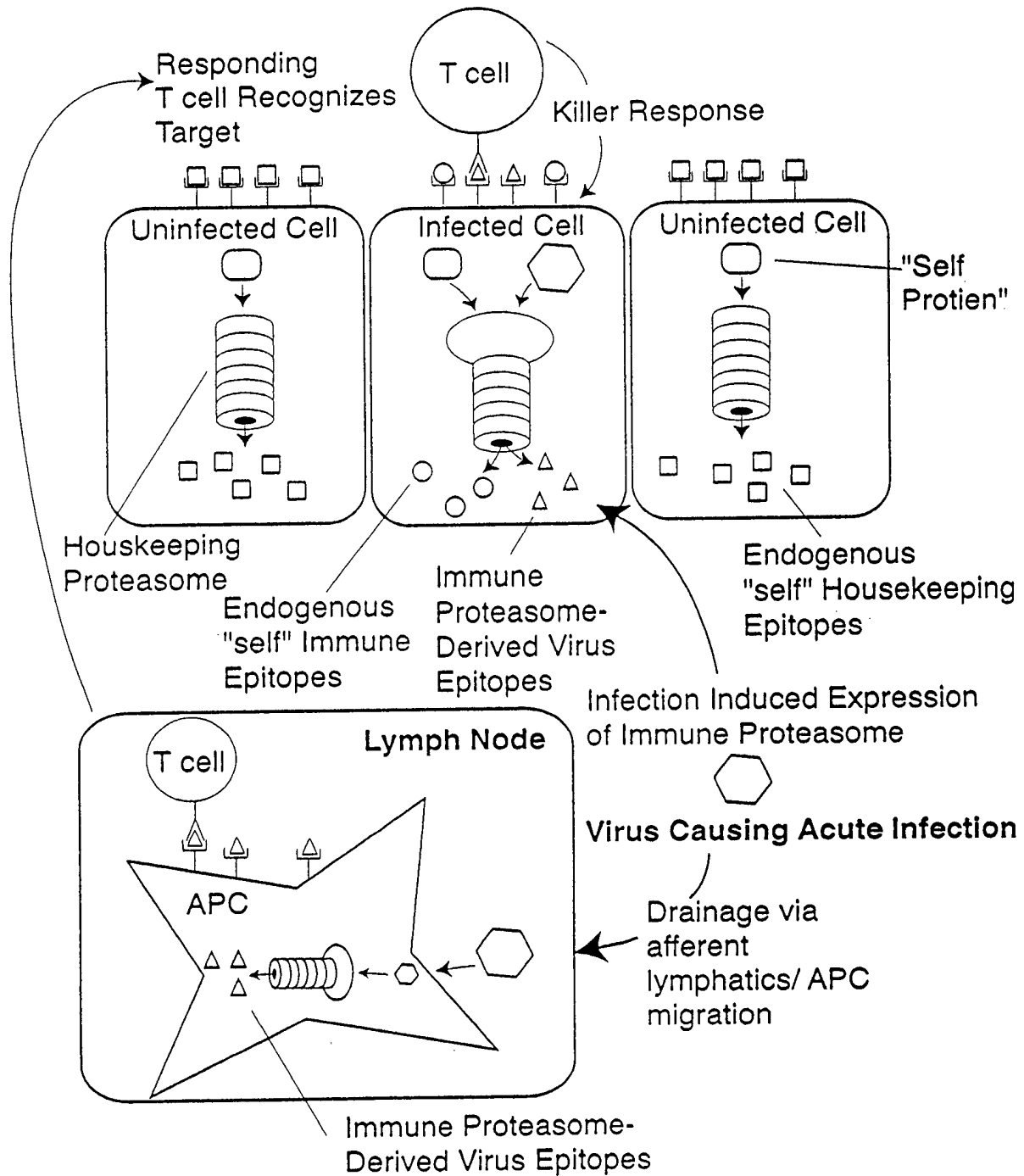


FIG. 3

T cell does not recognize Housekeeping Epitope (Tumor survives)

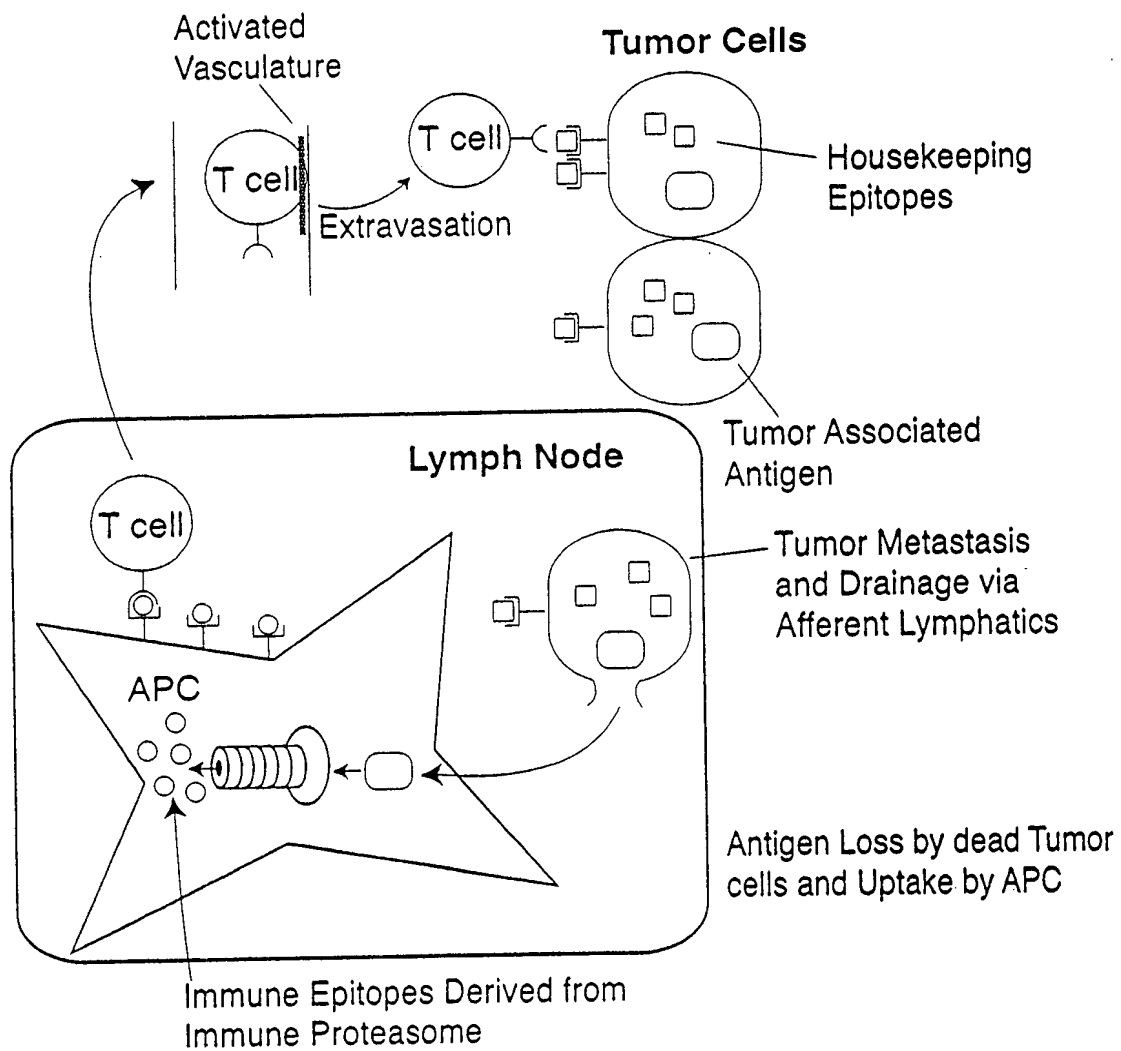


FIG. 4

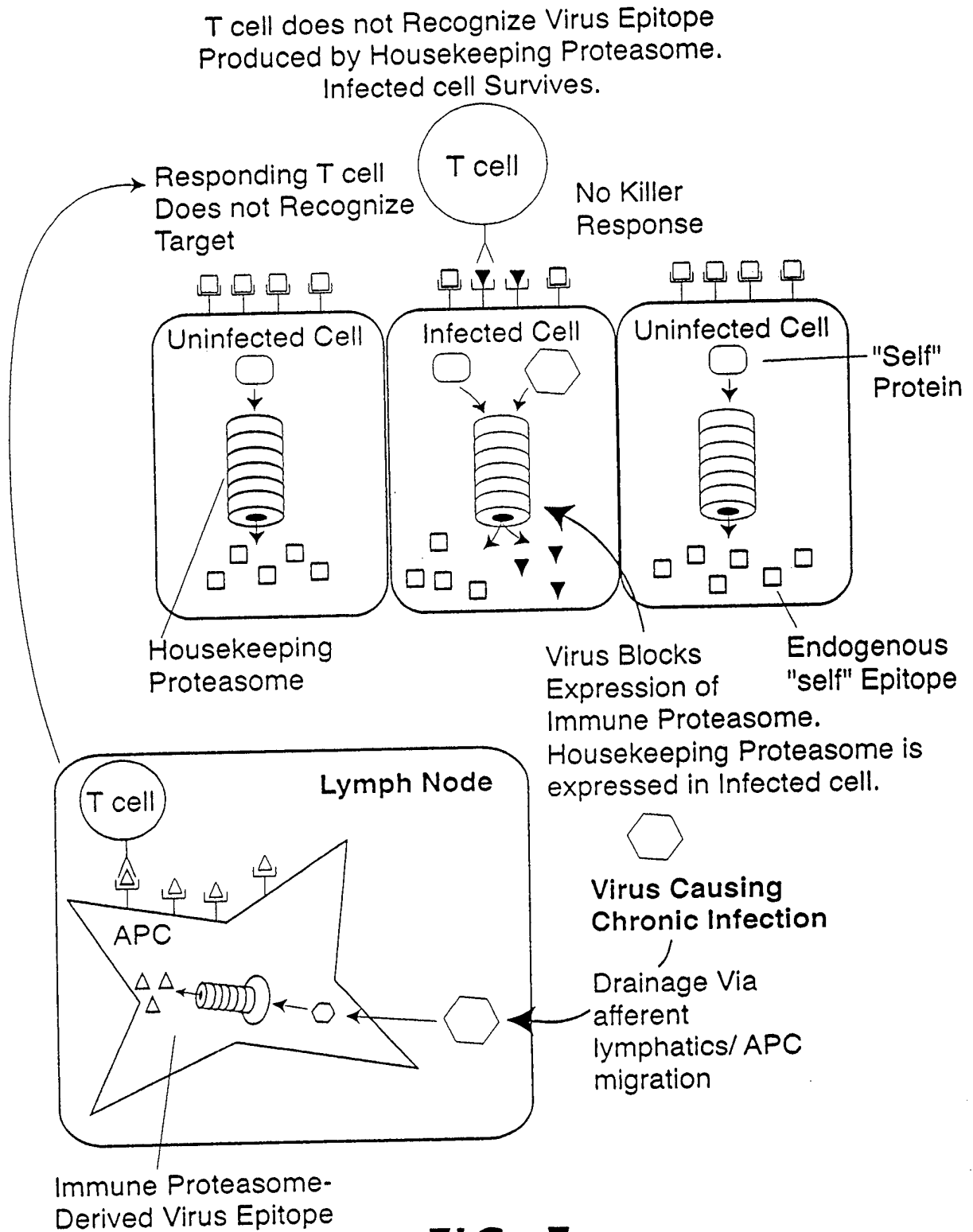


FIG. 5

IFN γ Production by T cell May Induce
Expression of Immune Proteasome
in some adjacent Tumor Cells. T cells
kill Tumor cells.

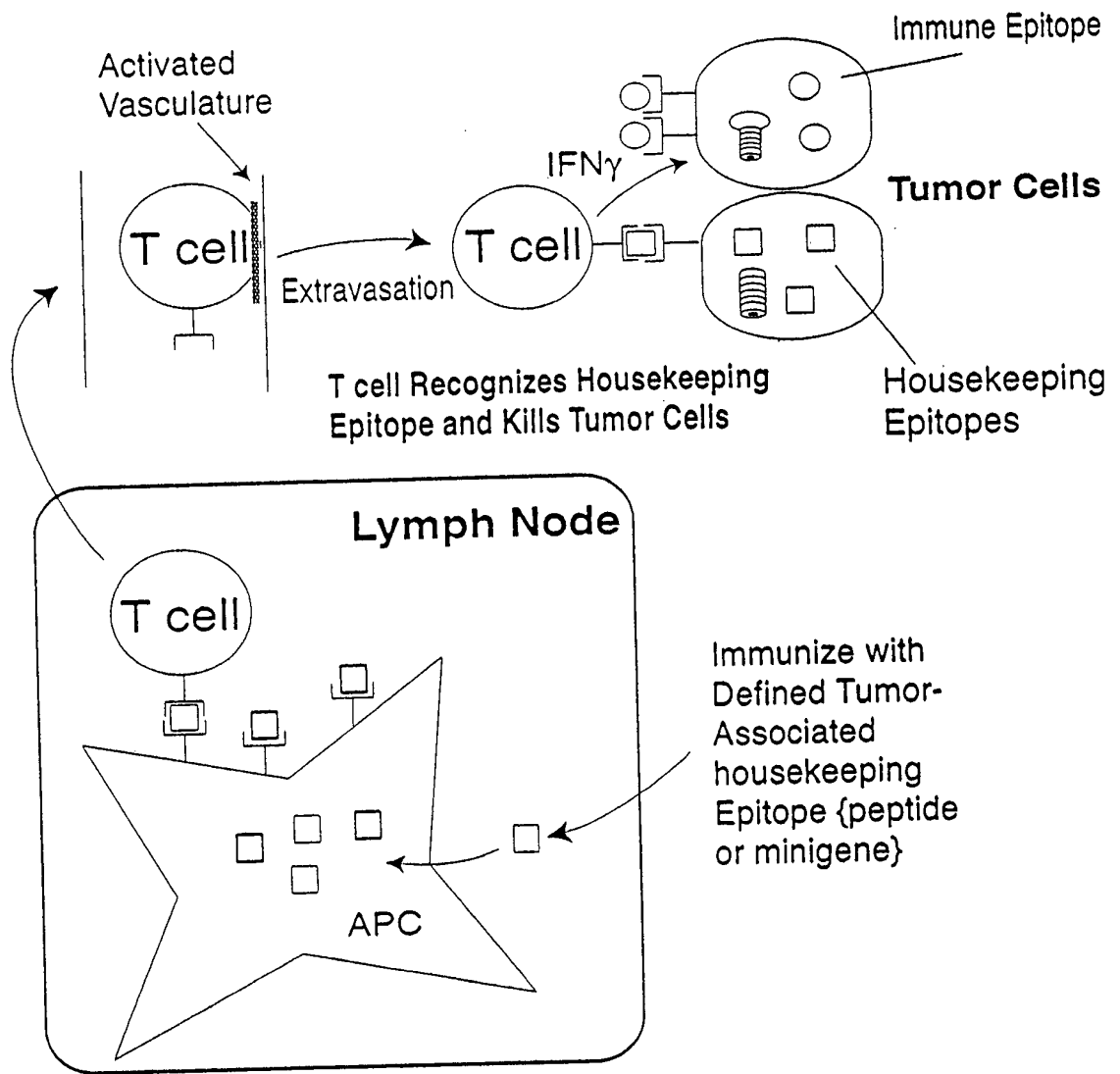


FIG. 6

FIG. 7

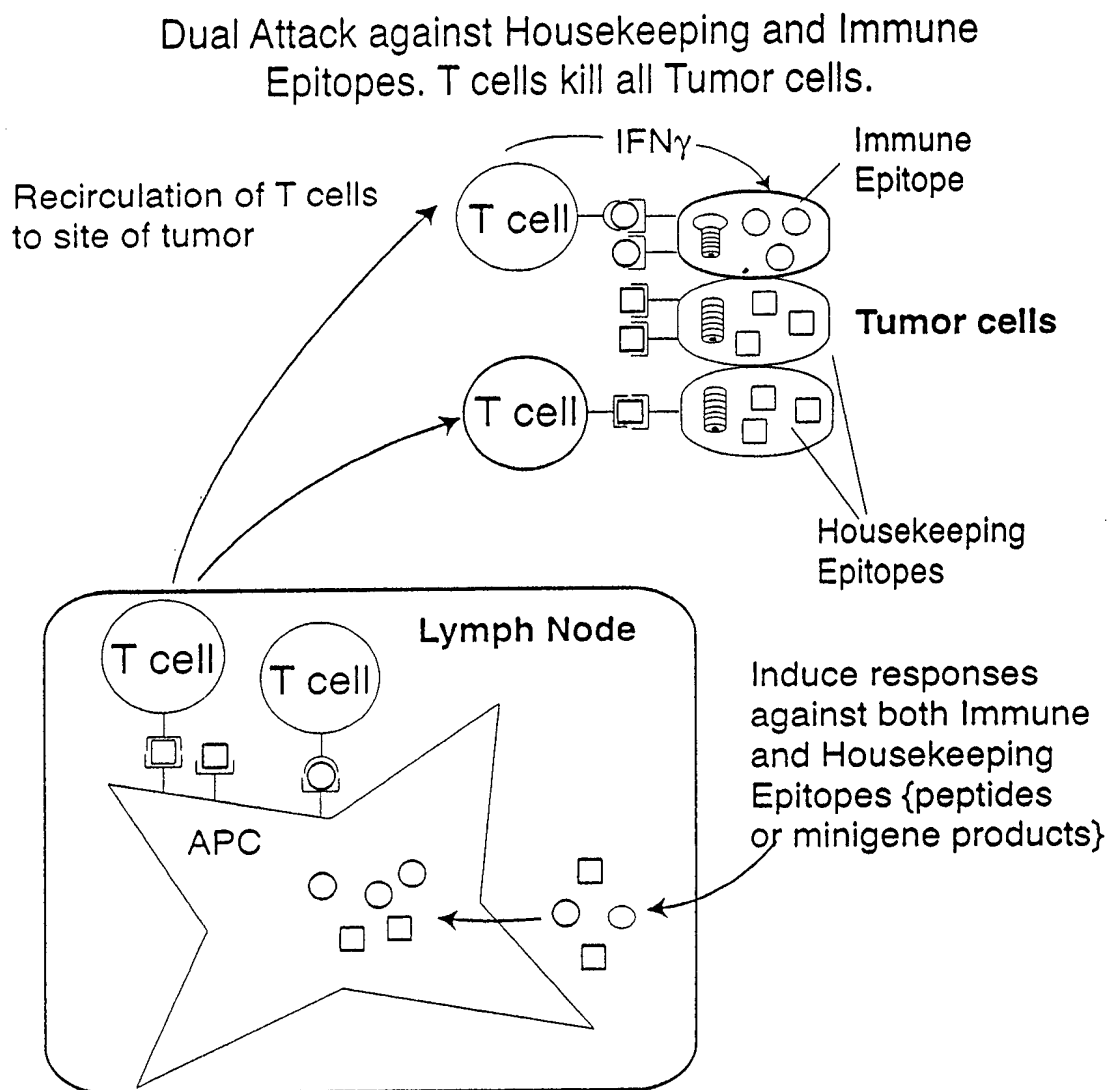


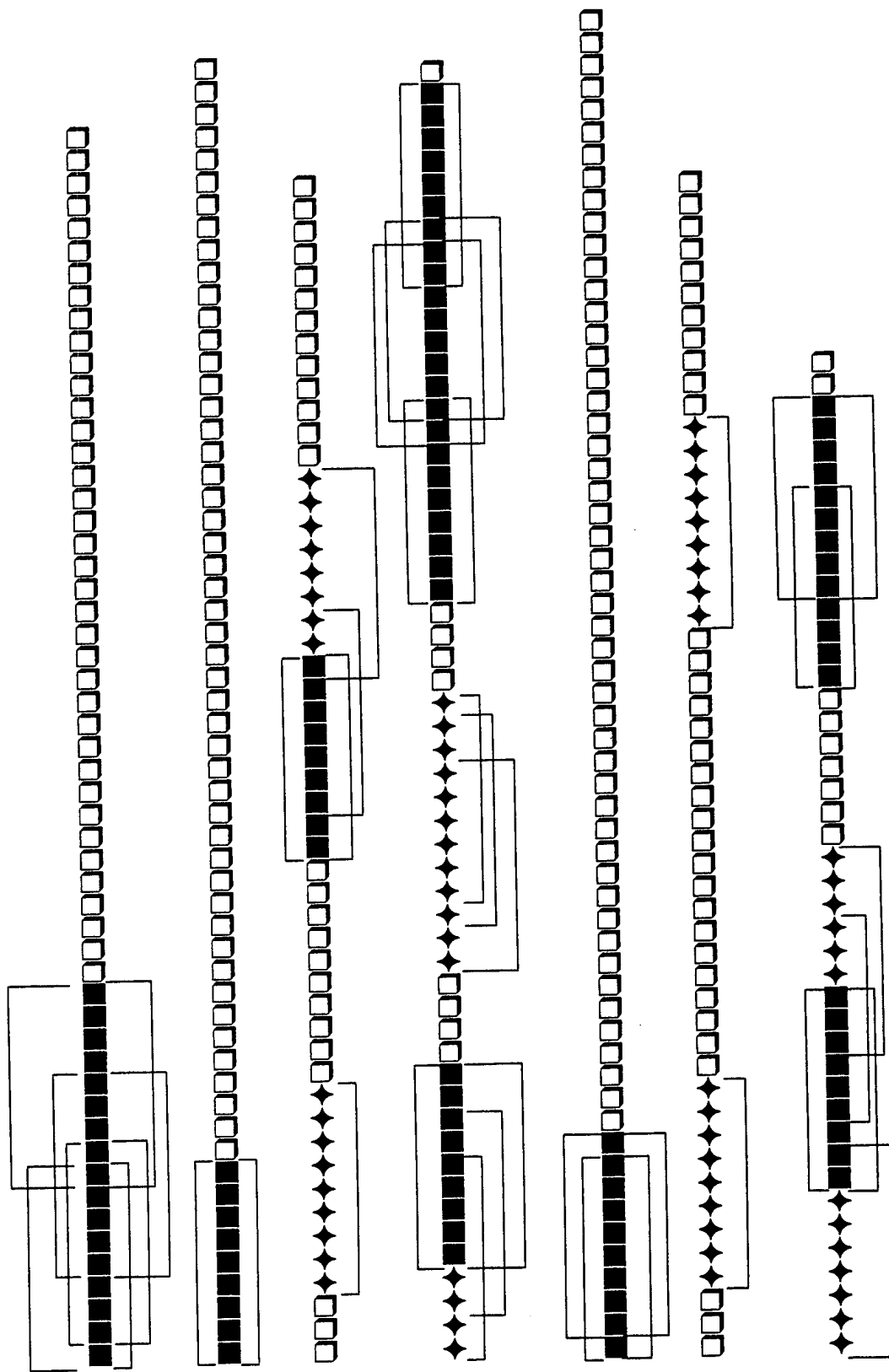
FIG. 8

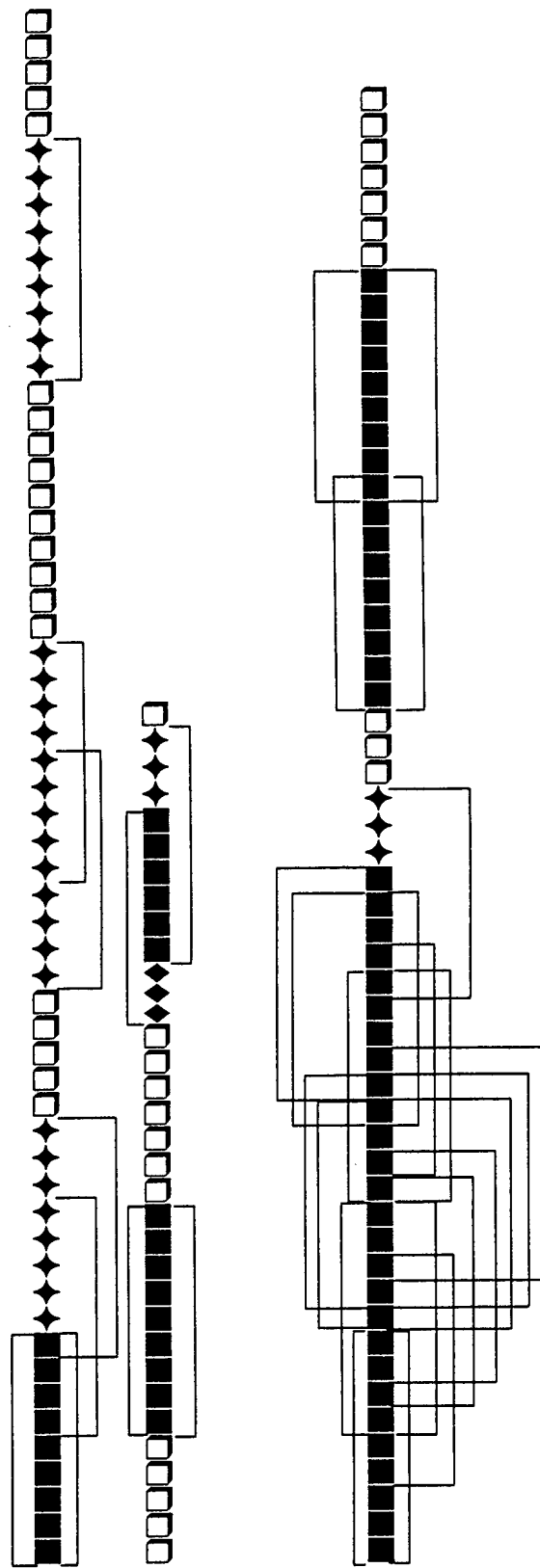
TYROSINASE

FIG. 9

FIG. 9A
FIG. 9B

FIG. 9A





- = an amino acid position not part of any epitope.
- = an amino acid position in an epitope according to both the SYFPEITHI and NIH algorithms.
- ◆ = an amino acid position in an epitope according to the NIH algorithm.
- ◆ = an amino acid position in an epitope according to the SYFPEITHI algorithm.

FIG. 9B

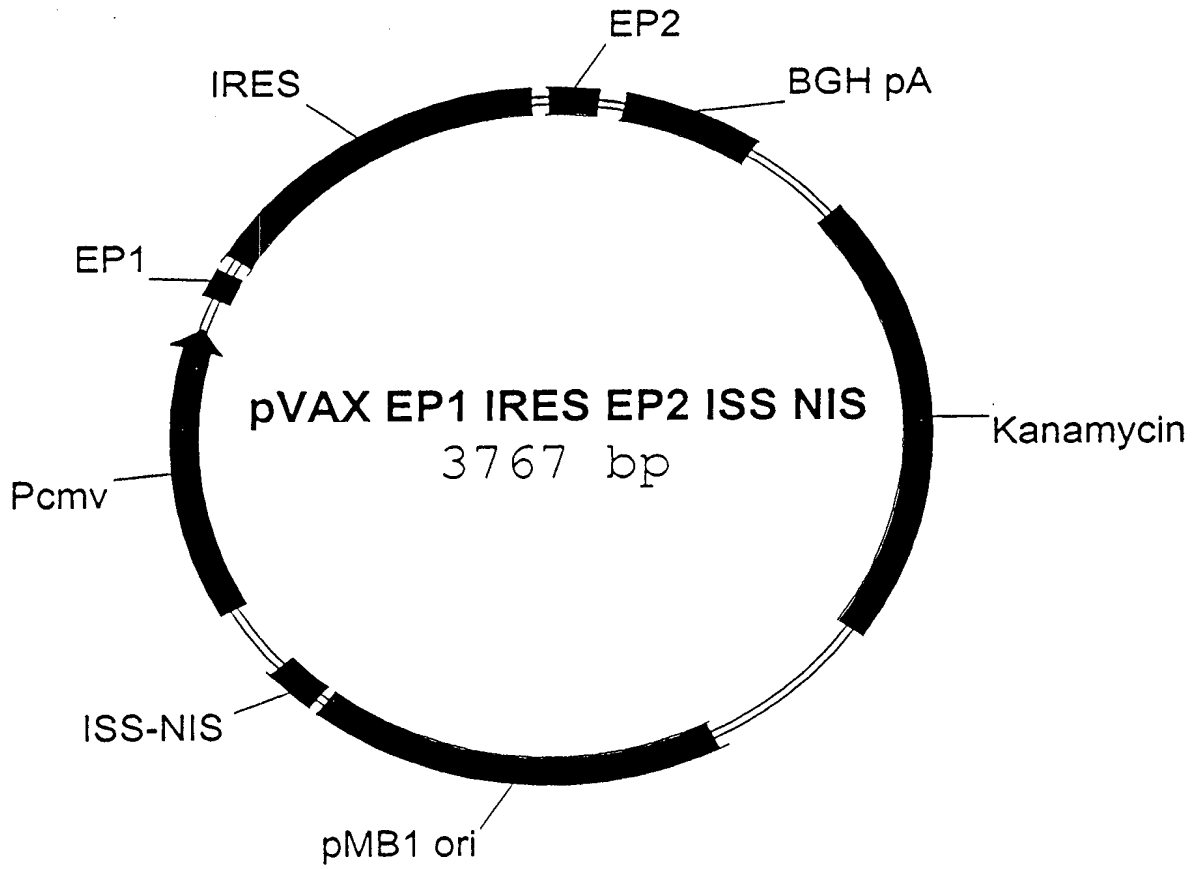


FIG. 10 A

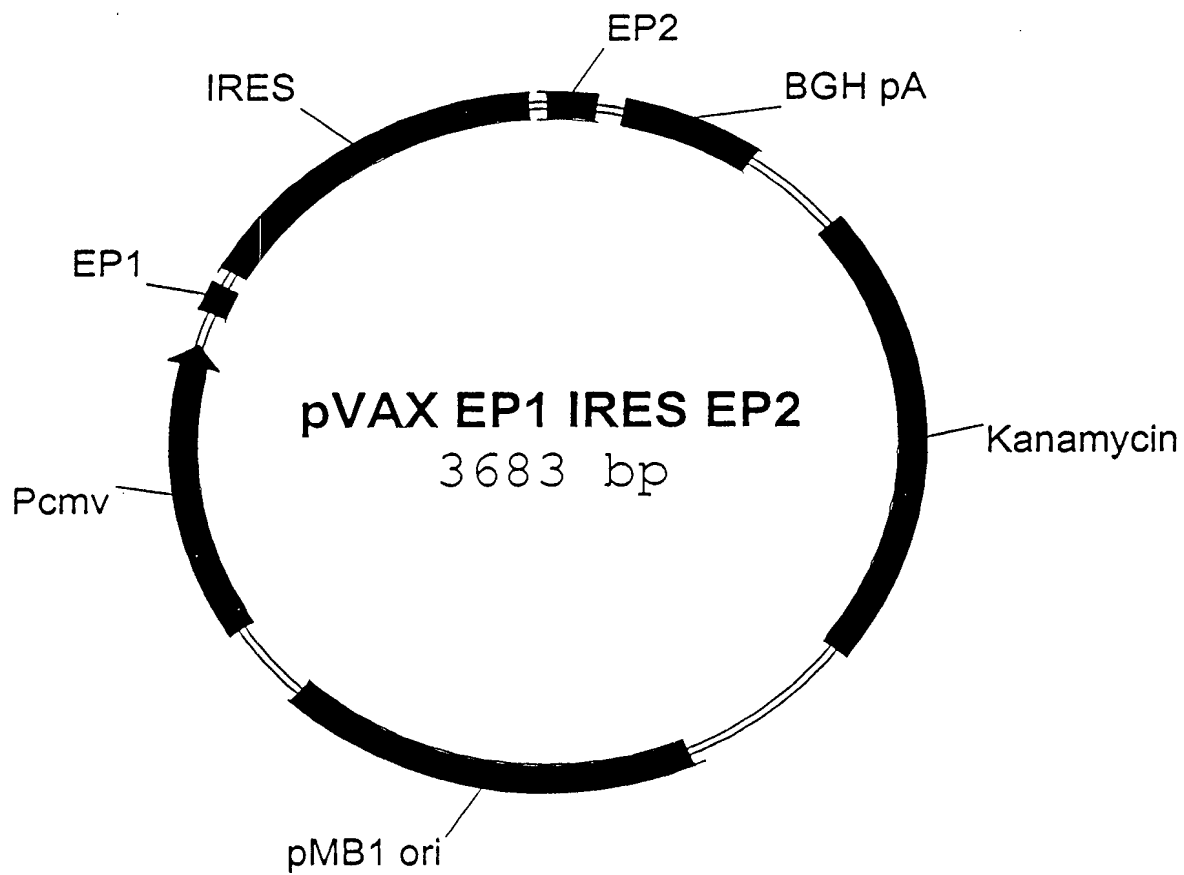


FIG. 10 B

10026056.120701

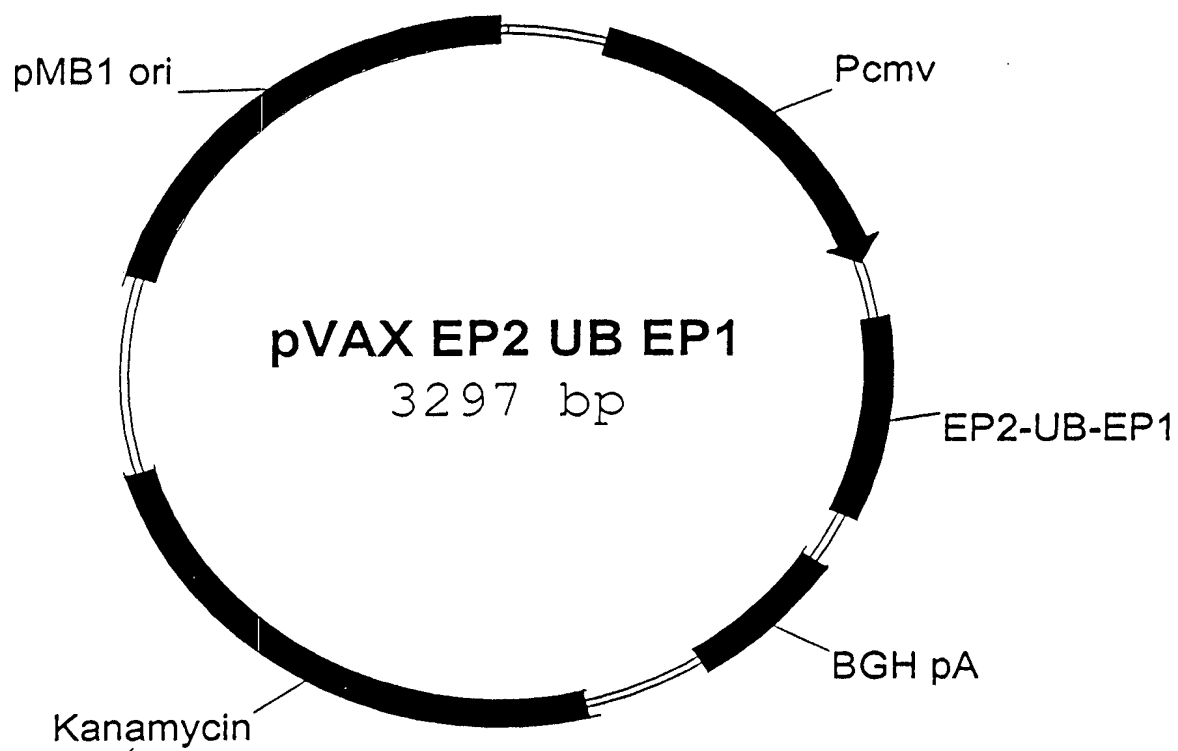


FIG. 11

10026066-120701

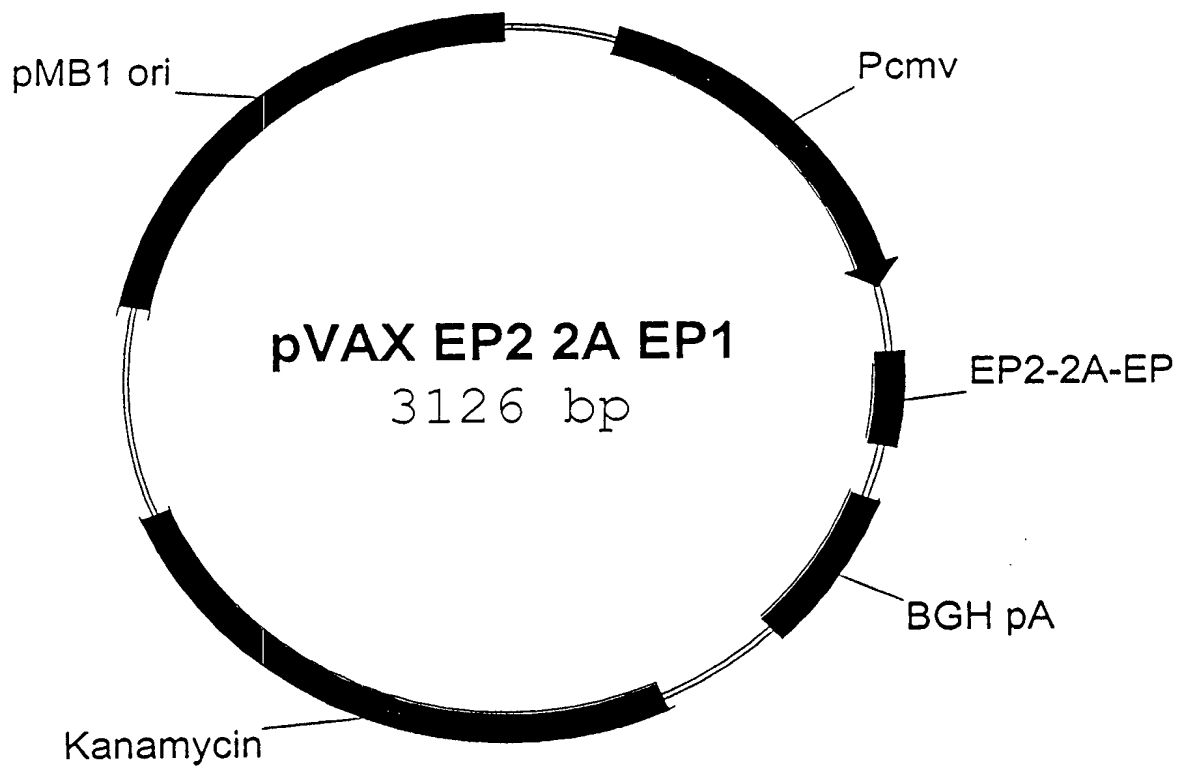


FIG. 12

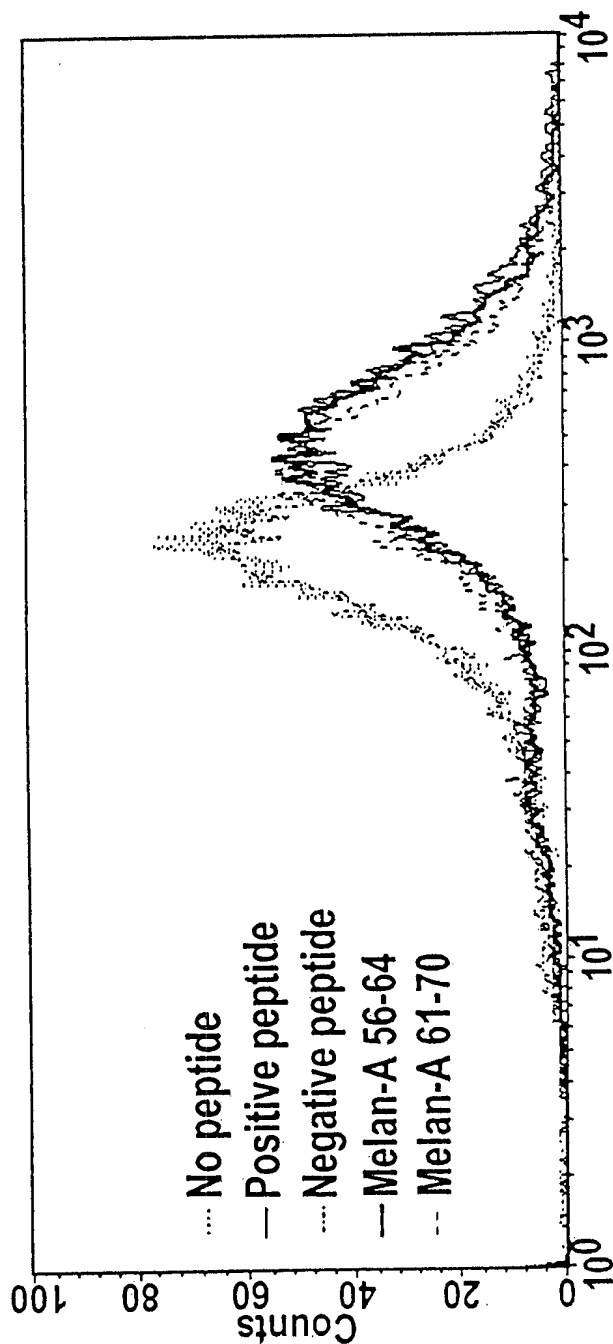


FIG. 13

FL1-Height

No Peptide				A2 Positive peptide			
File: Data.004				File: Data.005			
Total Events: 10000				Total Events: 10000			
Marker	Events	%	Total Mean	Marker	Events	%	Total Mean
All	10000	100.00	238.79	All	10000	100.00	604.21
Melan-A 56-64				Melan-A 61-70			
File: Data.009				File: Data.011			
Total Events: 10000				Total Events: 10000			
Marker	Events	%	Total Mean	Marker	Events	%	Total Mean
All	10000	100.00	535.86	All	10000	100.00	481.94
				Potitive peptide FI = 1.53			
				Melan-A 56-64 FI = 1.24			
				Melan-A 60-69 FI = 1.02			

Tyrosinase peptide 207-216 binds to human MHC I on T2 cells and enhances its expression

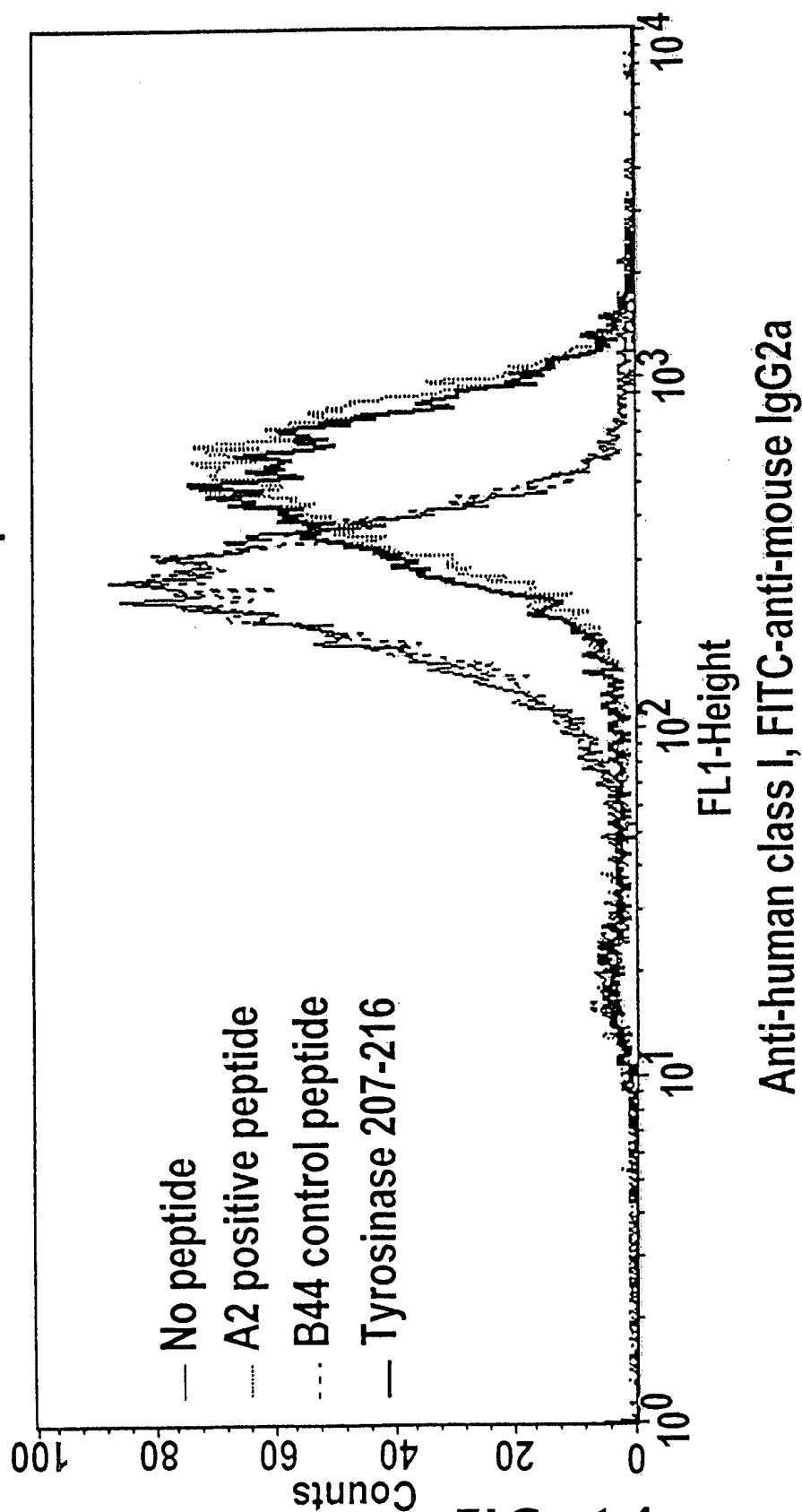
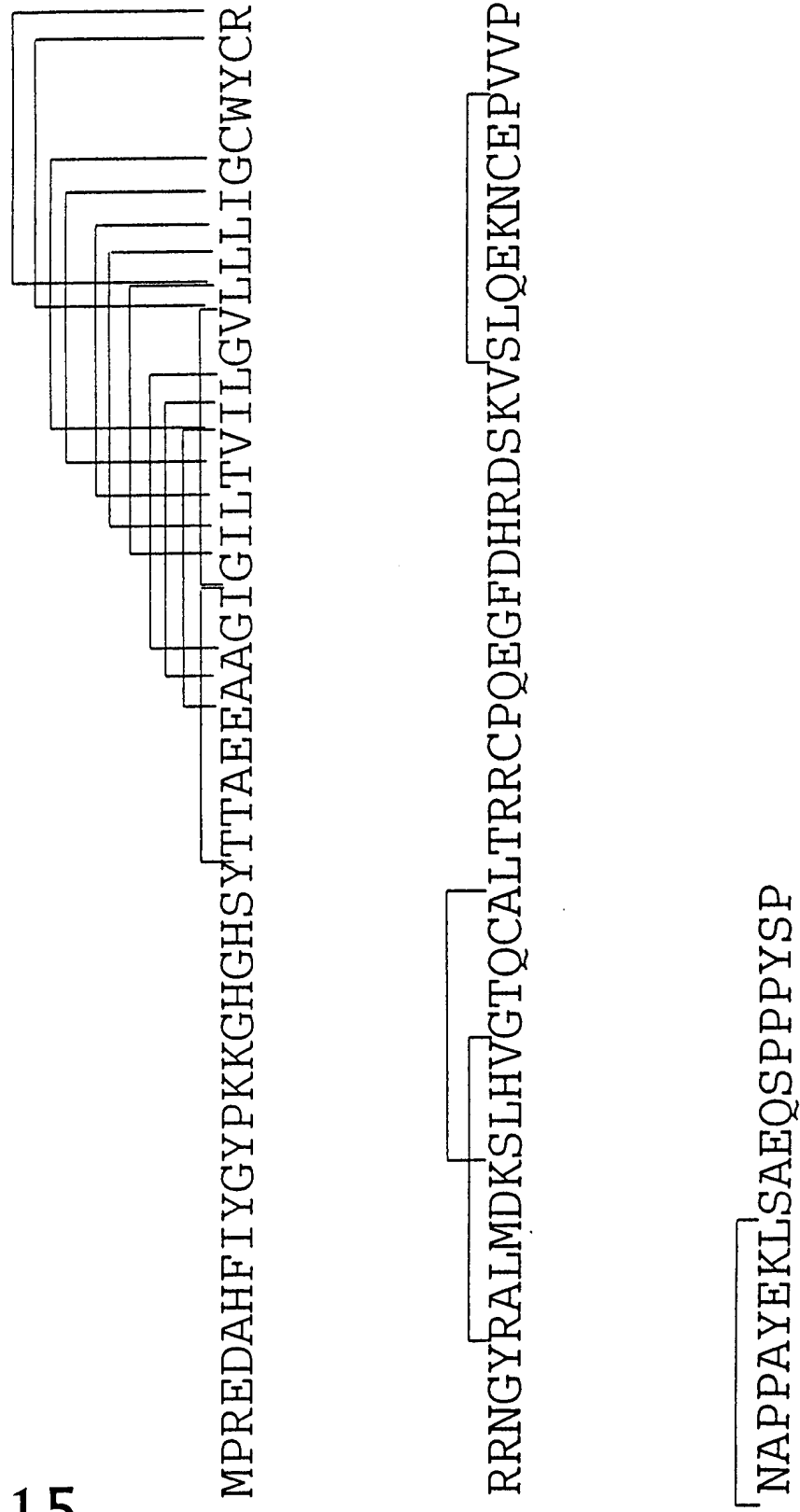


FIG. 14

Melan-A Class I HLA-A2 Epitopes

FIG. 15



SSX-2

MNGDDAFARRPTVGAQIPEKIQKAFDDIAKYFSKEEWEKM

KASEKIFVVMKRKYEAMTKLGFKATLPPFMCNKRAEDFQ

GNDLDNDPNRGNOVERPQMTFGRLOGISPKIMPKKPAEEG

NDSEEVPEASGPQNDGKELCPPGKPTTSEKIHRS GPKRG

EHAWTHRLRERKQLVIYEEISDPPEEDDE

FIG. 16

NY-ESO

MQAEGRTGG STGDADGPGG PGIPDGPCCN AGGPGGAGAT

GGRGPRGAGA ARASGPGGGA PRGPHGGAAS GLNGCCRCGA

RGPEs [RLLEFYLAM] PFATPMEAEELARRSLAQDAPPLPVP

[GVLLEFTVSGN] [ILTIRLTAA] DHR

[QLQLSISSCLQ] [QLSLLMWIT] [QCFLPV] [FLAQ] [PPSGQRR]

FIG. 17

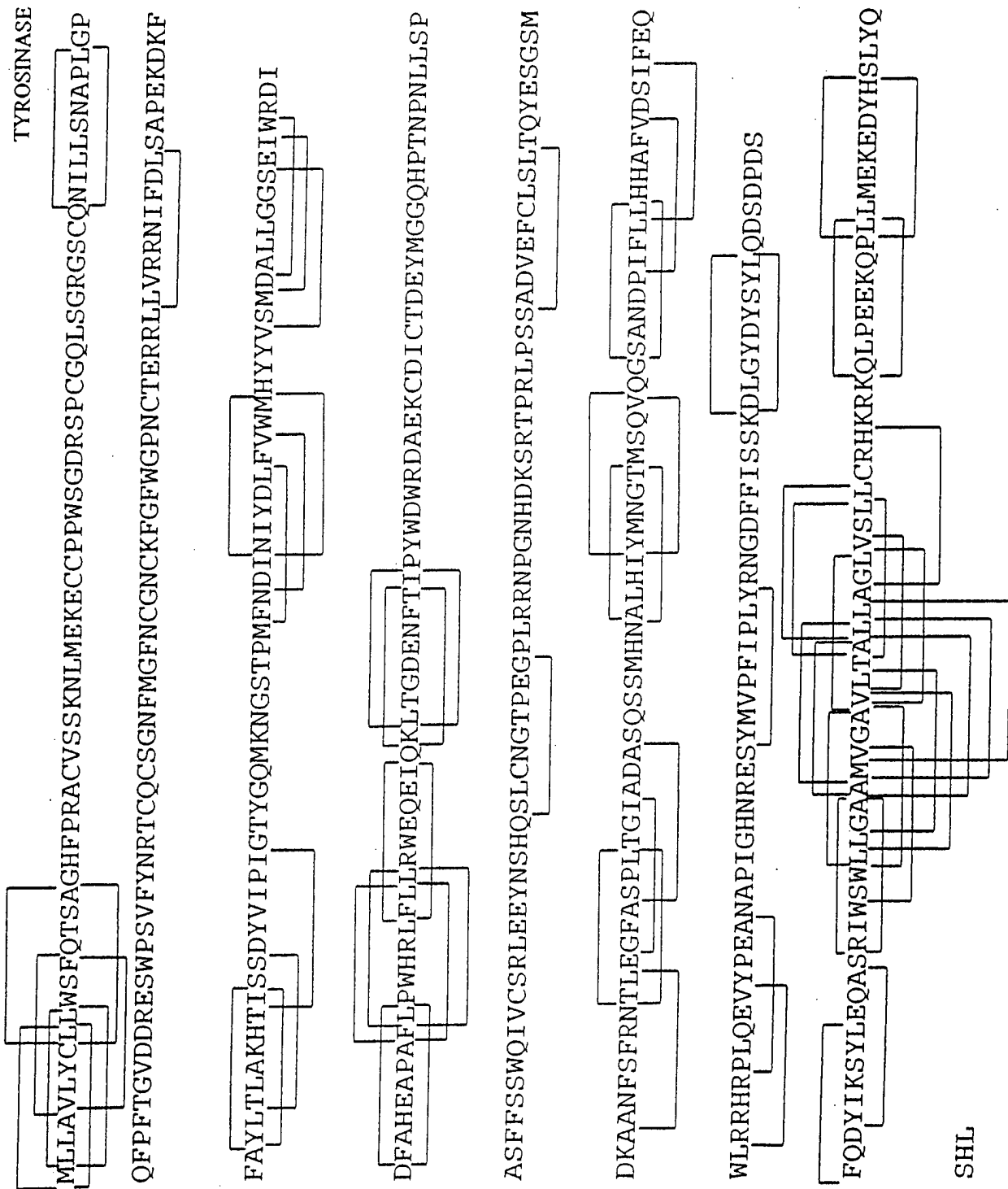


FIG. 18